

1647

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#21

RAW SEQUENCE LISTING

DATE: 09/09/2002

PATENT APPLICATION: US/09/386,450D

TIME: 09:18:44

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF4\09092002\I386450D.raw

5 <110> APPLICANT: Hotten, Gertrud  
 7 Neidhardt, Helge  
 9 Paulista, Michael  
 13 <120> TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATING FACTOR OF TGF-? Family  
 17 <130> FILE REFERENCE: 100564-09022  
 21 <140> CURRENT APPLICATION NUMBER: US 09/386,450D  
 23 <141> CURRENT FILING DATE: 1999-08-31  
 27 <150> PRIOR APPLICATION NUMBER: US 08/288,508  
 29 <151> PRIOR FILING DATE: 1994-08-10  
 33 <150> PRIOR APPLICATION NUMBER: DE P 43 26 829.3  
 35 <151> PRIOR FILING DATE: 1993-08-10  
 39 <150> PRIOR APPLICATION NUMBER: DE P 44 18 222.8  
 41 <151> PRIOR FILING DATE: 1994-05-25  
 45 <150> PRIOR APPLICATION NUMBER: DE P 44 20 157.5  
 47 <151> PRIOR FILING DATE: 1994-06-09  
 51 <160> NUMBER OF SEQ ID NOS: 41  
 55 <170> SOFTWARE: PatentIn version 3.0  
 59 <210> SEQ ID NO: 1  
 61 <211> LENGTH: 2703  
 63 <212> TYPE: DNA  
 65 <213> ORGANISM: Homo sapiens  
 69 <220> FEATURE:  
 71 <221> NAME/KEY: misc\_feature  
 73 <222> LOCATION: (1)..(2703)  
 75 <223> OTHER INFORMATION: coding region and non-translated regions for TGF-beta protein

MP-52

81 <400> SEQUENCE: 1  
 82 ccatggcctc gaaagggcag cgggtgatttt tttcacataa atatatcgca cttaaagtga 60  
 84 ttttagacagc atgacatcag agagtaatta aattggtttg ggttggaatt ccgtttccaa 120  
 86 ttcctgagtt caggtttgta aaagattttt ctgagcacct gcaggcctgt gagtgtgtgt 180  
 88 gtgtgtgtgt gtgtgtgtgt gtgtgtgtga agtattttca ctggaaagga ttcaaaacta 240  
 90 gggggaaaaa aaaactggag cacacaggca gcattacgcc attcttcctt cttggaaaaa 300  
 92 tccctcagcc ttatacaagc ctccttcaag ccctcagtca gttgtgcagg agaaaggggg 360  
 94 cggttggctt tctcctttca agaacgagtt attttcagct gctgactgga gacggtgcac 420  
 96 gtctggatac gagagcattt ccactatggg actggataca aacacacacc cggcagactt 480  
 98 caagagtctc agactgagga gaaagccttt ccttctgctg ctactgctgc tgccgctgct 540  
 100 tttgaaagtc cactcctttc atggtttttc ctgccaaacc agaggcacct ttgctgctgc 600  
 102 cgetgtttctc tttggtgtca ttcagcggct ggccagagga tgagactccc caaactcctc 660  
 104 actttctttgc tttggtacct ggcttggtctg gacctggaat tcatctgcac tgtgttggtg 720  
 106 gcccctgact tgggcccagag accccagggg accaggccag gattggccaa agcagaggcc 780  
 108 aaggagaggc cccccctggc ccggaacgtc ttcaggccag ggggtcacag ctatggtggg 840  
 110 ggggccacca atgccaatgc cagggcaaag ggaggcaccg ggcagacagg aggcctgaca 900  
 112 cagcccaaga aggatgaacc caaaaagctg cccccagac cgggcggccc tgaacccaag 960  
 114 ccaggacacc ctccccaac aaggcaggct acagcccga ctgtgacccc aaaaggacag 1020

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116 cttccccggag gcaaggcacc cccaaaagca ggatctgtcc ccagctcctt cctgctgaag 1080
118 aaggccaggg agcccgggccc cccacgagag cccaaggagc cgtttcgccc acccccctc 1140
120 acaccccacg agtacatgct ctgctgttac aggacgctgt ccgatgctga cagaaagga 1200
122 ggcaacagca gcgtgaagtt ggaggctggc ctggccaaca ccatcaccag ctttattgac 1260
124 aaagggcaag atgaccgagg tcccgtggtc aggaagcaga ggtacgtgtt tgacattagt 1320
126 gccctggaga aggatgggct gctggggggc gagctgcgga tcttgcgga gaagccctcg 1380
128 gacacggcca agccagcggc ccccgagggc gggcgggctg cccagctgaa gctgtccagc 1440
130 tgccccagcg gccggcagcc ggccctcctt ctggatgtgc gctccgtgcc aggcctggac 1500
132 ggatctggct gggagggtgt cgacatctgg aagctcttcc gaaactttaa gaactcggcc 1560
134 cagctgtgcc tggagctgga ggccctggga cggggcaggg ccgtggacct ccgtggcctg 1620
136 ggcttcgacc gcgccgcccg gcagggtccac gagaaggccc tgttctctgt gtttggccgc 1680
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140 accgtgtatg agtacctgtt cagccagcgg cgaaaacggc gggccccact ggccactcgc 1800
142 cagggcaagc gacccagcaa gaaccttaag gctcgtgca gtcggaaggc actgcatgtc 1860
144 aacttcaagg acatgggctg ggacgactgg atcatgcac cccttgagta cgaggctttc 1920
146 cactgcgagg ggctgtgcga gttcccattg cgtcccacc tggagccac gaatcatgca 1980
148 gtcattcaga ccctgatgaa ctccatggac cccgagtcca caccaccac ctgctgtgtg 2040
150 cccacgcggc tgagtcccat cagcatcctc ttcattgact ctgccaacaa cgtggtgtat 2100
152 aagcagtatg aggacatggt cgtggagtgc tgtggctgca ggtagcagca ctggccctct 2160
154 gtcttctcgg gtggcacatc ccaagagccc cttcctgcac tcctggaatc acagaggggt 2220
156 caggaagctg tggcaggagc atctacacag cttgggtgaa aggggattcc aataagcttg 2280
158 ctgctctctc gagtgtgact tgggctaaag gccccctttt atccacaagt tcccctggct 2340
160 gaggattgct gcccgctctg tgatgtgacc agtggcaggc acaggctcag ggagacagac 2400
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166 gtgccactgc ctctcaaat cacatttgtg cctggtgact tcctgtccct gggacagttg 2580
168 agaagctgac tgggcaagag tgggagagaa gaggagaggg cttggataga gttgaggagt 2640
170 gtgaggctgt tagactgtta gatttaaatg tatattgatg agataaaaag caaaactgtg 2700
172 cct

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175 &lt;210&gt; SEQ ID NO: 2

177 &lt;211&gt; LENGTH: 501

179 &lt;212&gt; TYPE: PRT

181 &lt;213&gt; ORGANISM: Homo sapiens

185 &lt;220&gt; FEATURE:

187 &lt;221&gt; NAME/KEY: DOMAIN

189 &lt;222&gt; LOCATION: (1)..(501)

191 &lt;223&gt; OTHER INFORMATION: TGF-beta protein MP-52 precursor

197 &lt;400&gt; SEQUENCE: 2

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199 Met Arg Leu Pro Lys Leu Leu Thr Phe Leu Leu Trp Tyr Leu Ala Trp
200 1 5 10 15
202 Leu Asp Leu Glu Phe Ile Cys Thr Val Leu Gly Ala Pro Asp Leu Gly
203 20 25 30
205 Gln Arg Pro Gln Gly Thr Arg Pro Gly Leu Ala Lys Ala Glu Ala Lys
206 35 40 45
208 Glu Arg Pro Pro Leu Ala Arg Asn Val Phe Arg Pro Gly Gly His Ser
209 50 55 60
211 Tyr Gly Gly Gly Ala Thr Asn Ala Asn Ala Arg Ala Lys Gly Gly Thr
212 65 70 75 80
214 Gly Gln Thr Gly Gly Leu Thr Gln Pro Lys Lys Asp Glu Pro Lys Lys

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215				85					90				95
217	Leu	Pro	Pro	Arg	Pro	Gly	Gly	Pro	Glu	Pro	Lys	Pro	Pro
218				100					105				110
220	Gln	Thr	Arg	Gln	Ala	Thr	Ala	Arg	Thr	Val	Thr	Pro	Lys
221				115					120				125
223	Pro	Gly	Gly	Lys	Ala	Pro	Pro	Lys	Ala	Gly	Ser	Val	Pro
224				130					135				140
226	Leu	Leu	Lys	Lys	Ala	Arg	Glu	Pro	Gly	Pro	Pro	Arg	Glu
227	145								150				155
229	Pro	Phe	Arg	Pro	Pro	Pro	Ile	Thr	Pro	His	Glu	Tyr	Met
230													160
232	Tyr	Arg	Thr	Leu	Ser	Asp	Ala	Asp	Arg	Lys	Gly	Gly	Asn
233				165					170				175
235	Lys	Leu	Glu	Ala	Gly	Leu	Ala	Asn	Thr	Ile	Thr	Ser	Phe
236				180					185				190
238	Gly	Gln	Asp	Asp	Arg	Gly	Pro	Val	Val	Arg	Lys	Gln	Arg
239				195					200				205
241	Asp	Ile	Ser	Ala	Leu	Glu	Lys	Asp	Gly	Leu	Leu	Gly	Ala
242	225								210				215
244	Ile	Leu	Arg	Lys	Lys	Pro	Ser	Asp	Thr	Ala	Lys	Pro	Ala
245									220				225
247	Gly	Gly	Arg	Ala	Ala	Gln	Leu	Lys	Leu	Ser	Ser	Cys	Pro
248				230					235				240
250	Gln	Pro	Ala	Ser	Leu	Leu	Asp	Val	Arg	Ser	Val	Pro	Gly
251				245					250				255
253	Ser	Gly	Trp	Glu	Val	Phe	Asp	Ile	Trp	Lys	Leu	Phe	Arg
254				260					265				270
256	Asn	Ser	Ala	Gln	Leu	Cys	Leu	Glu	Leu	Glu	Ala	Trp	Glu
257	305								280				285
259	Ala	Val	Asp	Leu	Arg	Gly	Leu	Gly	Phe	Asp	Arg	Ala	Ala
260				290					295				300
262	His	Glu	Lys	Ala	Leu	Phe	Leu	Val	Phe	Gly	Arg	Thr	Lys
263				310					315				320
265	Leu	Phe	Phe	Asn	Glu	Ile	Lys	Ala	Arg	Ser	Gly	Gln	Asp
266				325					330				335
268	Val	Tyr	Glu	Tyr	Leu	Phe	Ser	Gln	Arg	Arg	Lys	Arg	Arg
269				340					345				350
271	Ala	Thr	Arg	Gln	Gly	Lys	Arg	Pro	Ser	Lys	Asn	Leu	Lys
272	385								355				360
274	Ser	Arg	Lys	Ala	Leu	His	Val	Asn	Phe	Lys	Asp	Met	Gly
275				365					370				375
277	Trp	Ile	Ile	Ala	Pro	Leu	Glu	Tyr	Glu	Ala	Phe	His	Cys
278				380					385				390
280	Cys	Glu	Phe	Pro	Leu	Arg	Ser	His	Leu	Glu	Pro	Thr	Asn
281				390					395				400
283	Ile	Gln	Thr	Leu	Met	Asn	Ser	Met	Asp	Pro	Glu	Ser	Thr
284				405					410				415
286	Cys	Cys	Val	Pro	Thr	Arg	Leu	Ser	Pro	Ile	Ser	Ile	Leu
287	465								415				420
				420					425				430
				435					430				435
				440					445				450
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289 Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val Val Glu
290                               485                               490                               495
292 Ser Cys Gly Cys Arg
293                               500
295 <210> SEQ ID NO: 3
297 <211> LENGTH: 24
299 <212> TYPE: DNA
C--> 301 <213> ORGANISM: Artificial
305 <220> FEATURE:
307 <221> NAME/KEY: misc_feature
309 <222> LOCATION: (1)..(24)
311 <223> OTHER INFORMATION: adapter primer
317 <400> SEQUENCE: 3
318 agaattcgca tgccatgggc gacg                                     24
321 <210> SEQ ID NO: 4
323 <211> LENGTH: 23
325 <212> TYPE: DNA
327 <213> ORGANISM: Homo sapiens
331 <220> FEATURE:
333 <221> NAME/KEY: misc_feature
335 <222> LOCATION: (1)..(23)
337 <223> OTHER INFORMATION: MP-52 internal primer
343 <400> SEQUENCE: 4
344 cttgagtacg aggctttcca ctg                                     23
347 <210> SEQ ID NO: 5
349 <211> LENGTH: 24
351 <212> TYPE: DNA
C--> 353 <213> ORGANISM: Artificial
357 <220> FEATURE:
359 <221> NAME/KEY: misc_feature
361 <222> LOCATION: (1)..(24)
363 <223> OTHER INFORMATION: adapter primer
369 <400> SEQUENCE: 5
370 attcgcatgc catggctcgac gaag                                     24
373 <210> SEQ ID NO: 6
375 <211> LENGTH: 23
377 <212> TYPE: DNA
379 <213> ORGANISM: Homo sapiens
383 <220> FEATURE:
385 <221> NAME/KEY: misc_feature
387 <222> LOCATION: (1)..(23)
389 <223> OTHER INFORMATION: MP-52 internal primer
395 <400> SEQUENCE: 6
396 ggagcccacg aatcatgcag tca                                     23
399 <210> SEQ ID NO: 7
401 <211> LENGTH: 23
403 <212> TYPE: DNA
405 <213> ORGANISM: Homo sapiens
409 <220> FEATURE:

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RAW SEQUENCE LISTING  
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Input Set : A:\PTO.VSK.txt  
 Output Set: N:\CRF4\09092002\I386450D.raw

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411 <221> NAME/KEY: misc_feature
413 <222> LOCATION: (1)..(23)
415 <223> OTHER INFORMATION: MP-52 internal primer
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422 acagcaggtg ggtggtgtgg act 23
425 <210> SEQ ID NO: 8
427 <211> LENGTH: 44
429 <212> TYPE: DNA
C--> 431 <213> ORGANISM: Artificial
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437 <221> NAME/KEY: misc_feature
439 <222> LOCATION: (1)..(44)
441 <223> OTHER INFORMATION: primer composed of oligo dT and an adapter sequence
447 <400> SEQUENCE: 8
448 agaattcgca tgccatgggc gacgaagctt tttttttttt tttt 44
451 <210> SEQ ID NO: 9
453 <211> LENGTH: 20
455 <212> TYPE: DNA
457 <213> ORGANISM: Homo sapiens
461 <220> FEATURE:
463 <221> NAME/KEY: misc_feature
465 <222> LOCATION: (1)..(20)
467 <223> OTHER INFORMATION: MP-52 internal primer
473 <400> SEQUENCE: 9
474 ccagcagccc atccttctcc 20
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483 <213> ORGANISM: Homo sapiens
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491 <222> LOCATION: (1)..(24)
493 <223> OTHER INFORMATION: MP-52 internal primer
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503 <210> SEQ ID NO: 11
505 <211> LENGTH: 24
507 <212> TYPE: DNA
509 <213> ORGANISM: Homo sapiens
513 <220> FEATURE:
515 <221> NAME/KEY: misc_feature
517 <222> LOCATION: (1)..(24)
519 <223> OTHER INFORMATION: MP-52 internal primer
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526 actaatgtca aacacgtacc tctg 24
529 <210> SEQ ID NO: 12
531 <211> LENGTH: 10
533 <212> TYPE: DNA
C--> 535 <213> ORGANISM: Artificial

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/386,450D

DATE: 09/09/2002  
TIME: 09:18:45

Input Set : A:\PT0.VSK.txt  
Output Set: N:\CRF4\09092002\I386450D.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:13; Line(s) 571

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,5,8,12,19,30,41

## VERIFICATION SUMMARY

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Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF4\09092002\I386450D.raw

L:301 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3  
L:353 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5  
L:431 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8  
L:535 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12  
L:832 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19  
L:1118 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:30  
L:1404 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:41